

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 9, 2002, 01:18:04 ; Search time 10687.2 seconds
(without alignments)
3033.262 Million cell updates/sec

Title: US-08-913-842-2

Perfect score: 1965
Sequence: 1 AAGCTTCAAGTAACTCTCTG.....TGAACACAAAGAAATG 1965

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

1 number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

GenBankl:*

- 1: gb_da:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_om:*
- 20: em_or:*
- 21: em_ov:*
- 22: em_pat:*
- 23: em_ph:*
- 24: em_pl:*
- 25: em_ro:*
- 26: em_sts:*
- 27: em_sy:*
- 28: em_un:*
- 29: em_vi:*
- 30: em_htgo_hum:*
- 31: em_htgo_inv:*
- 32: em_htgo_rtd:*
- 33: em_htg_hum:*
- 34: em_htg_inv:*
- 35: em_htg_rtd:*
- 36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	178	9.1	1319	8	VIREXT5	D16458 V.angularis
2	115.2	5.9	136098	2	AC006970	AC006970 Homo sapi
3	114.8	5.8	12029	3	AE001422	AE001422 Homo sapi
4	114.6	5.8	86827	3	PFMAL3P5	AL0034556 Plasmodiu
5	112.4	5.7	136098	9	AC006970	AC006970 Homo sapi
6	112.2	5.7	259474	9	HDAC004605	AC004605 Homo sapi
7	112	5.7	196152	2	AC079796	AC079796 Homo sapi
8	111.6	5.7	158398	2	AC011146	AC011146 Homo sapi
9	110.2	5.6	86827	3	PFMAL3P5	AL0034556 Plasmodiu
10	110	5.6	161991	2	AC055860	AC055860 Homo sapi
11	109.6	5.6	158398	2	AC011146	AC011146 Homo sapi
12	109.2	5.6	115218	9	HS159A1	AL034397 Human DNA
13	108.8	5.5	193302	2	AC021992	AL031746 Plasmodiu
14	108.6	5.5	67970	3	PFMAL1P3	AL031746 Plasmodiu
15	108.4	5.5	142339	2	AL390835	AL390835 Homo sapi
16	108.2	5.5	175223	2	AC004617	AC004617 Homo sapi
17	108	5.5	14867	3	AE001398	AE001398 Plasmodiu
18	108	5.5	157176	2	AC084716	AC084716 Homo sapi
19	107.6	5.5	326924	2	AC093082	AC093082 Homo sapi
20	107.4	5.5	39347	9	AL135806	AL135806 Homo sapi
21	107.4	5.5	140455	2	AL356793	AL356793 Homo sapi
22	107.4	5.5	201312	2	AC067900	AC067900 Homo sapi
23	107.2	5.5	156133	2	AL593856	AL593856 Homo sapi
24	107	5.4	176174	9	AC007483	AC007483 Homo sapi
25	106.8	5.4	128603	2	AL356272	AL356272 Homo sapi
26	106.6	5.4	172805	9	AC066608	AC066608 Homo sapi
27	106.6	5.4	178087	9	AC005089	AC005089 Homo sapi
28	106.4	5.4	4601	3	DMU01584	U11584 Drosophila
29	106.4	5.4	19517	3	DMU037541	U37541 Drosophila
30	106.4	5.4	104992	2	AC005504	AC005504 Plasmodiu
31	106.4	5.4	169546	2	AC004157	AC004157 Plasmodiu
32	106.2	5.4	120029	2	HS282810	AL132672 Homo sapi
33	106.2	5.4	199335	2	AC092665	AC092665 Homo sapi
34	106	5.4	106763	9	AP002091	AP002091 Homo sapi
35	105.8	5.4	205094	2	CNS01RHO	AL162191 Homo sapi
36	105.6	5.4	142239	2	AL390835	AL390835 Homo sapi
37	105.6	5.4	194212	2	AC092148	AC092148 Homo sapi
38	105.4	5.4	36977	3	PFMAL1P3	AL031746 Plasmodiu
39	105.4	5.4	67970	3	PFMAL1P3	AL031746 Plasmodiu
40	105.4	5.4	161286	2	AC025120	AC025120 Homo sapi
41	105.4	5.4	175223	9	AC004617	AC004617 Homo sapi
42	105.2	5.4	326924	2	AC093082	AC093082 Homo sapi
43	104.8	5.3	169794	2	AC004688	AC004688 Plasmodiu
44	104.8	5.3	172666	2	AC046181	AC046181 Homo sapi
45	104.8	5.3	185385	2	AL589943	AL589943 Homo sapi

ALIGNMENTS

RESULT 1

VIREXT5 1319 bp mRNA 01-FEB-2000
LOCUS V.angularis mRNA for endo-xyloglucan transferase, complete cds.
DEFINITION D16458
ACCESSION D16458
VERSION D16458.1 GI:457572
KEYWORDS endo-glycanotransferase; endo-xyloglucan transferase; extracellular protein; glycosylated protein; molecular grafting between xyloglucan polymers; novel glycosyltransferase.
SOURCE Vigna angularis seedlings cDNA to mRNA.
ORGANISM Vigna.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.

REFERENCE 1 (bases 1 to 1319)
Okazawa,K., Sato,Y., Nakagawa,T., Asada,K., Kato,I., Tomita,E. and Nishitani,K.
Molecular cloning and cDNA sequencing of endoxyloglucan transferase, a novel class of glycosyltransferase that mediates

JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL

molecular grafting between matrix polysaccharides in plant cell walls
J. Biol. Chem. 268 (34), 25364-25368 (1993)
2 (bases 1 to 1319)
Nishitani, K.
Submitted (17-JUN-1993) Kazuhiko Nishitani, Kagoshima University,
College of Liberal Arts, Department of Biology, Kagoshima,
Kagoshima 890, Japan (E-mail: nishitani@cla.kagoshima-u.ac.jp,
Tel: 0992-85-8938, Fax: 0992-85-8946)
Submitted (17-JUN-1993) to DBJ by:

COMMENT

Kazuhiko Nishitani
Department of Biology
College of Liberal Arts
Kagoshima University
Kagoshima 890
Japan
Phone: 0992-85-8938
Fax: 0992-85-8946.

FEATURES
source

Location/Qualifiers
1. 1319

/organism="Vigna angularis"
/db_xref="taxon:3914"
/dev_stage="seedlings"
176. 235
/gene="text"
176. 1054
/gene="text"
176. 1054
/gene="text"
/codon_start=1
/product="endo-xylolucan transferase"
/protein_id="BA03925.1"
/db_xref="GI:469510"

BASE COUNT
ORIGIN

399 a 276 c 261 g 383 t

Query Match 9.1%; Score 178; DB 8; Length 1319;
Best Local Similarity 100.0%; Pred. No. 5.7e-14;
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1788 ATGGAACACAAATACCAATCTCAATCAATGACATTTAATTAATTCAGTTA 1847
1 ATGGAACACAAATACCAATCTCAATCAATGACATTTAATTAATTCAGTTA 60
1848 AAAGTATGATCAGAACAGCAGTGAAGTATGATTAAGCGGTATAGTCGAGCAG 1907
61 AAAGTATGATCAGAACAGCAGTGAAGTATGATTAAGCGGTATAGTCGAGCAG 120
1908 AGTGTGCTCTATATATACCTTTGGAATGACACAAAGTTGAACACAAAGAAATG 1965
21 AGTGTGCTCTATATATACCTTTGGAATGACACAAAGTTGAACACAAAGAAATG 178

RESULT 2

AC006970 136098 bp DNA PRI 27-SEP-2000
LOCUS Homo sapiens clone RP4-725G10, complete sequence.
DEFINITION AC006970
ACCESSION AC006970
VERSION
WORDS
GTG. GI:10312289
human.
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 136098)
AUTHORS Waterston, R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
2 (bases 1 to 136098)
REFERENCE
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (05-MAR-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
3 (bases 1 to 136098)
REFERENCE
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (27-SEP-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Sep 27, 2000 this sequence version replaced gi:8838025.
Center project name: H.DJ0725G10.

COMMENT

FEATURES
source

Location/Qualifiers
1. 136098
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP4-725G10"

BASE COUNT
ORIGIN

38294 a 29779 c 30262 g 37763 t

Query Match 5.9%; Score 115.2; DB 9; Length 136098;
Best Local Similarity 47.3%; Pred. No. 2.3e-06;
Matches 510; Conservative 0; Mismatches 558; Indels 10; Gaps 5;

823 TAATTAAGATGCTACCTATGCAATCATGCTTAATGTAATATGTAATGATTAAGTACCT 882
112840 TAT 112899
883 TGAATATTCCTGTTGTTCCGACATACCTCAATATGAAAAAAGAAAAACACTTGA 942
112900 TAT 112959
943 GAACCTTTTAAAGAT 1002
112960 AAT 113019
1003 GAAATATACATACAAACGATTTGAAAGTATATCCGATGGAATTTGTTTACATACAG 1062
113020 TAT 113079
1063 AAAATTCACCAAAATTAAGTCCATCTTACGATTAATATATATATATATATATATAT 1122
113080 TAT 113139
1123 CTTCGGTTTCACGCTTCCCATGTTTACATGTAATCACTTCATTTATTTTATG 1182
113140 TAT 113199
1183 ---TTTCATGCTCTTATACCATCCCTTTATTTTACATTTATATATACCATCTCCCA 1239
113200 ATATTTAT 113259
1240 ATATCTTATATTTCTTAAGATATATGTAACATTTATAT -CTAATGATACATTAAGTAA 1298
113260 ATATTTAT 113319
1299 GTAATATTCATAGAAATAATAAATGATCTTTTCAAGAAACACACACTTAATATATA 1358
113320 ATTTAT 113379
1359 TATAGAAAGTATTTACATTTTTCCTTAACATGTCACATATTTACACTCTGCAAG 1418
113380 TTTAT 113439
1419 AAAAAGTGTAGAAAT 1478

Query Match	9.28;	Score 173.2;	DB 2;	Length 205094;
Best Local Similarity	46.68;	Pred. No. 4.1e-11;		
Matches 804; Conservative	0;	Mismatches 898;	Indels 22;	Gaps 7

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OW nucleic - nucleic search, using sw model

Run on: January 8, 2002, 19:07:28 ; Search time 10687.2 Seconds

(without alignments)
2894.334 Million cell updates/sec

Title: US-08-913-842-1

Perfect score: 1875
Sequence: 1 AACCTTTTGCACATTTTG.....TGAAACACAAAGAAAAATG 1875

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

GenEmbl: *
1: gb.ba:*
2: gb.htg:*
3: gb.in:*
4: gb.om:*
5: gb.ov:*
6: gb.pat:*
7: gb.ph:*
8: gb.pl:*
9: gb.pr:*
10: gb.ro:*
11: gb.sts:*
12: gb.sy:*
13: gb.un:*
14: gb.vi:*
15: em.ba:*
16: em.fun:*
17: em.hum:*
18: em.in:*
19: em.om:*
20: em.or:*
21: em.ov:*
22: em.pat:*
23: em.ph:*
24: em.pl:*
25: em.ro:*
26: em.sts:*
27: em.sy:*
28: em.un:*
29: em.vi:*
30: em.hugo.hum:*
31: em.hugo.inv:*
32: em.hugo.rod:*
33: em.htg.hum:*
34: em.htg.inv:*
35: em.htg.rod:*
36: em.htg.other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	178	9.5	1319	8	VIREXTS
2	173.2	9.2	205094	2	CNS01RHO
3	159.4	8.5	86827	3	PFMAL3P5
4	156.6	8.4	158398	2	AC011146
5	155.4	8.3	4601	3	DMU1584
6	155.4	8.3	19517	3	DMU37541
7	154.2	8.2	4601	3	DMU1584
8	154.2	8.2	19517	3	DMU37541
9	153.4	8.2	14867	3	DMU01398
10	151.6	8.1	156933	2	AC026839
11	151.4	8.1	183584	9	AC012492
12	151.2	8.1	143331	9	AC091214
13	150.4	8.0	14867	3	AE001398
14	150.4	8.0	67970	3	PFMAL1P3
15	149.2	8.0	176174	9	AC007483
16	148.6	7.9	67970	3	PFMAL1P3
17	147.6	7.9	104992	2	AC005504
18	147.6	7.9	169546	2	AC004157
19	146	7.8	86827	3	PFMAL3P5
20	144.8	7.7	104992	2	AC005504
21	144.8	7.7	169546	2	AC004157
22	143.6	7.7	158398	2	AC011146
23	141.8	7.6	175223	9	AC092304
24	141.2	7.5	326924	2	AC093082
25	138.6	7.4	172666	2	AC046181
26	138.4	7.4	36977	2	AC092304
27	138.2	7.4	173349	2	AL596253
28	137.8	7.3	188930	2	AC091742
29	137	7.3	218078	2	AC068138
30	136.6	7.3	176174	9	AC007483
31	136.6	7.3	326924	2	AC093082
32	136	7.3	199551	2	AC006281
33	134.8	7.2	188930	2	AC091742
34	134.6	7.1	103649	2	AL445219
35	133.6	7.1	36977	2	AC092304
36	133.4	7.1	106650	9	AC007708
37	133	7.1	173349	2	AL596253
38	132.8	7.0	136098	9	AC006970
39	132	7.0	172666	2	AC046181
40	131.2	7.0	181581	7	AC026621
41	130.8	7.0	259474	9	HUAC004605
42	130.4	6.9	14001	3	PFMAL1P3
43	128.6	6.9	106763	9	AP002091
44	128.6	6.8	142239	2	AL390835
45	128				

ALIGNMENTS

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE
1	VIREXTS	V. angularis mRNA for endo-xyloglucan transferase, complete cds.	D16458	D16458.1	GI:457572	endo-glycanotransferase; endo-xyloglucan transferase; extracellular protein; glycosylated protein; molecular grafting between xyloglucan polymers; novel glycosyltransferase.	Vigna angularis seedlings cDNA to mRNA.	1 (bases 1 to 1319)	Okazawa,K., Sato,Y., Nakagawa,T., Asada,K., Kato,I., Tomita,E. and Nishitani,I.K.	Molecular cloning and cDNA sequencing of endoxyloglucan transferase, a novel class of glycosyltransferase that mediates